REMARKS

The Office Action has been carefully reviewed. No claim is allowed. Claims 8, 17, 37 and newly added dependent claims 46-55 presently appear in this application, with claims 37 being withdrawn from consideration by the examiner, and define patentable subject matter warranting their allowance. Reconsideration and allowance are hereby respectfully solicited.

Withdrawn claim 26 is now cancelled without prejudice to refiling in a divisional application.

The personal interview between the undersigned and the examiner on March 13, 2012, is gratefully acknowledged. The cloning of the SpaA of the SE-9 strain and the correspondence between Fujisawa strain SpaA of SEQ ID NO:2 and the SpaA encoded by the nucleotide sequence of SEQ ID NO:7 from the SE-9 strain were discussed. This discussion at the interview and the proposed amendments to the claims are incorporated into the remarks below.

Dependent claims 46-55, while not discussed at the interview, are newly added merely so that the different specific variants recited in claims 8 and 17 are each recited individually in a separate dependent claim.

Claims 8 and 17 have been rejected under 35 USC 112, second paragraph as being indefinite. The examiner states

that the claims recite that the SpaA protein has the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:7, but that SEQ ID NO:7, according to the specification, depicts a portion of a full-length nucleotide sequence of the SpaA gene derived from the SE-9 strain. The examiner asserts that the amino acid sequence encoded by SEQ ID NO:7 does not comprise the amino acids to be substituted at positions 531, 214, 253, 69, 154 and 278 as claimed. Furthermore, the examiner asks which 207 amino acid residues at the C-terminus are being deleted. This rejection is obviated by the amendments to the claims as discussed below.

The cloning of SpaA and ΔSpaA from the SE-9 strain is disclosed in Example 1 in the paragraph bridging pages 30 and 31 of the present specification. The present specification at page 21, lines 6-14 further discloses:

> SEQ ID NO:1 depicts a full-length nucleotide sequence of SpaA gene derived from Fujisawa strain whereas SEQ ID NO:2 depicts an amino acid sequence of a full-length SpaA protein derived from Fujisawa strain encompassing a signal peptide. SEQ ID NO:7 depicts a portion of a full-length nucleotide sequence of SpaA gene derived from SE-9 strain, which corresponds to the sequence of from the 107th to 1854th nucleotide residues in SEQ ID NO:1.

The attached nucleotide and amino acid alignment compares SpaA from the Fujisawa strain (SEQ ID NO:1 and SEQ ID NO:2, the top two lines, are the nucleotide and amino acid

sequences, respectively) with the SpaA from the SE-9 strain (SEQ ID NO:7 as partial nucleotide sequence being presented as the third line with the encoded amino acid sequence presented immediately underneath as the fourth line). The features of the primers (SEQ ID NOs:3, 4 and 5), the NcoI site, and the nucleotides corresponding to the 79th, 107th, 1260th, 1854th, and 1881st nucleotide positions of SEQ ID NO:1 from the Fujisawa strain, discussed in the above-referenced sections of the present specification, are also shown in the attached nucleotide and amino acid alignment.

The present claims are amended to recite amino acid substitutions at residue positions numbered on the basis of the full length SpaA protein of SEQ ID NO:2 (from the Fujisawa strain) which encompasses the signal peptide. As taught at page 21 of the specification, SEQ ID NO:7 corresponds to nucleotides 107 to 1854 of SEQ ID NO:1. Such a nucleotide sequence alignment is quite clear from the attached alignment, where considerable sequence identity exists between the two sequences at both the nucleotide and amino acid levels. The amino acid sequence identity is shown in the alignment with shading.

The residue positions recited in the claims as the ones which may be substituted correspond to residues at

residue positions 69, 154, 203, 214, 253, 278 and 531 of SEQ ID NO:2. Note that the residues at positions 69, 154, 203, 214, 253 and 278 based on the numbering of SEQ ID NO:2 are identical between the aligned amino acid sequences, with only the residue at position 531 being different. From the nucleotide and amino acid sequence alignment, it is clear and unambiguous which residue positions based on SEQ ID NO:2 the recited substitutions would be made.

As for the recitation in claim 8 of "207 amino acid residues at the C-terminus of the SpaA protein are deleted", this is amended to instead read "the C-terminal 206 amino acid residues of the SpaA protein of the SE9 strain of *Erysipelothrix rhusiopathiae* are deleted." By reciting that it is the "C-terminal 206 residues", applicants clarify that the residues deleted are the last 206 residues of the SpaA protein. This particular amendment also corrects the number of residues from "207" to "206". Although page 22, lines 6-10, discloses that 207 residues are deleted at the C-terminal, it can be clearly seen from the alignment attached hereto that a ΔSpaA protein encoded up until the 1260th nucleotide (as also taught in the section on page 22, lines 6-10 of the specification) is lacking the last 206 residues (residues 421-626) of the SpaA protein. The disclosure of "207" residues mistakenly calculated the stop codon at nucleotides 1879-1881

as encoding an amino acid residue, which it obviously does not.

The amendments to the claims, as supported by the disclosures and teachings in the present specification and as discussed with the examiner at the interview, obviate this rejection.

Reconsideration and withdrawal of the rejection are therefore respectfully requested.

As the amendments to the claims are believed to obviate the indefiniteness rejection and place the elected product claims in condition for allowance, rejoinder of the withdrawn method claim 37, dependent from allowable claim 8, is respectfully requested.

In view of the above, the claims comply with 35 U.S.C. §112 and define patentable subject matter warranting their allowance. Favorable consideration and early allowance are earnestly urged.

Respectfully submitted,

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Appendix

The Appendix includes the following item(s):

- Nucleotide and amino acid sequence alignment between SEQ ID NOs:1 and 7, and between SEQ ID NO:2 and the amino acid sequence encoded by SEQ ID NO:7